OM nucleic - nucleic search, using sw model

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                GenCore version 5.1.6
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Run on:     October  9, 2005, 02:08:12 ; Search time 5587 Seconds
                                    (without alignments)
                        11344.088 Million cell updates/sec

Title:          US-09-993-180-1_COPY_68_1375
Perfect score:  1308
Sequence:       1 atgcaaggacaggcaggag.........aaaatcccactaaatcctag 1308

Scoring table:  IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched:       4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters:        9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      GenEmbl:*
                 1: gb_ba:*
                 2: gb_htg:*
                 3: gb_in:*
                 4: gb_om:*
                 5: gb_ov:*
                 6: gb_pat:*
                 7: gb_ph:*
                 8: gb_pl:*
                 9: gb_pr:*
                10: gb_ro:*
                11: gb_sts:*
                12: gb_sy:*
                13: gb_un:*
                14: gb_vi:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1308	100.0	1743	6	AX191430	AX191430 Sequence
2	1308	100.0	1743	6	AX454638	AX454638 Sequence
3	1308	100.0	1743	6	AX491116	AX491116 Sequence
4	1308	100.0	1743	6	AX697167	AX697167 Sequence
5	1308	100.0	1743	9	AY358700	AY358700 Homo sapi
6	1308	100.0	1766	6	AX675079	AX675079 Sequence
7	1298.4	99.3	1313	6	AR541803	AR541803 Sequence
8	1298.4	99.3	1710	6	AR560132	AR560132 Sequence
9	1295.2	99.0	1787	9	AY220118	AY220118 Sequence
10	1270.4	97.1	1581	6	AX392981	AX392981 Sequence
11	1270.4	97.1	1759	6	AX355862	AX355862 Sequence
12	1263.4	96.6	1329	6	AX135904	AX135904 Sequence
13	1262.4	96.5	1580	6	AX392967	AX392967 Sequence
14	1244.4	95.1	1254	6	CQ735615	CQ735615 Sequence
15	1182.8	90.4	1194	6	AX135908	AX135908 Sequence
16	1097	83.9	1346	9	AY185496	AY185496 Homo sapi
17	1073.4	82.1	1548	9	AY220120	AY220120 Homo sapi
18	872	66.7	1156	9	AY185497	AY185497 Homo sapi
19	869.8	66.5	1489	9	AY220121	AY220121 Homo sapi
20	733.6	56.1	1451	9	AY220119	AY220119 Homo sapi
21	647.2	49.5	147505	9	CNS01DTA	AL112708 Human chr
22	647.2	49.5	181004	9	CNS01DTY	AL132990 Human chr
c 23	537.8	41.1	1365	9	BC020747	BC020747 Homo sapi
24	537.8	41.1	1872	9	AX409610	AX409610 Sequence
25	537.8	41.1	1872	9	HUMTBG	M14091 Human thyro
26	536.6	41.0	1280	4	AP204928	AF204928 Bos tauru
27	534.6	40.9	1432	6	AR531797	AR531797 Sequence
28	525.4	40.2	1395	4	OATBG	X69795 O.aries mRN
29	519.6	39.7	1785	6	CQ716276	CQ716276 Sequence
30	518.4	39.6	1284	6	AF204929	AF204929 Sus scrof
31	488.6	37.4	1714	6	AX401745	AX401745 Sequence
32	488.6	37.4	1714	10	RATTBGAA	M63991 Rat thyroxi
33	476.8	36.5	1388	10	AY575783	AY575783 Mus muscu
34	373.2	28.5	1428	6	AX642662	AX642662 Sequence
35	373.2	28.5	1428	9	HUMAACTA	J05176 Human alpha
36	373.2	28.5	1466	6	BD176851	BD176851 A method
37	373.2	28.5	1466	6	AX770543	AX770543 Sequence
38	373.2	28.5	1466	9	AF089747	AF089747 Homo sapi
39	373.2	28.5	1522	6	CQ802318	CQ802318 Sequence
40	373.2	28.5	1522	6	CQ814554	CQ814554 Sequence
41	373.2	28.5	1522	6	AX642661	AX642661 Sequence
42	373.2	28.5	1528	6	CQ720070	CQ720070 Sequence
43	373.2	28.5	1592	9	BC010530	BC010530 Homo sapi
44	373.2	28.5	1603	9	BC003559	BC003559 Homo sapi
45	373.2	28.5	2480	6	AX747885	AX747885 Sequence

ALIGNMENTS

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RESULT 1
AX191430
LOCUS       AX191430               1743 bp    DNA     linear   PAT 15-AUG-2001
DEFINITION  Sequence 5 from Patent WO0149715.
ACCESSION   AX191430
VERSION     AX191430.1  GI:15209638
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ashkenazi,A.J., Goddard,A., Gurney,A.L., Napier,M.A., Watanabe,C.K.
            and Wood,W.I.
  TITLE     Methods and compositions for inhibiting neoplastic cell growth
  JOURNAL   Patent: WO 0149715-A 5 12-JUL-2001;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1..1743
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Query Match             100.0%;  Score 1308;  DB 6;  Length 1743;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1308;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ATGCAAGGACAGGGCAGGAGAAGAGGAACCTGCAAAGACACATATTTGTTCCAAAATGGCA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6 ATGCAAGGACAGGGCAGGAGAAGAGGAACCTGCAAAGACACATATTTGTTCCAAAATGGCA 65

Qy     61 TCTTACCTTTATGGAGTACTCTTTGCTTGTGGCCTCGTGTTGCGTGTCC 120
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db     66 TCTTACCTTTATGGAGTACTCTTTGCTTGTGGCCTCGTGTTGCGTGTCC 125

Qy    121 CCGGCCAATGCCCCAGTGCATACCCCGCCCTTCCTCCACAAAGAGCACCCCTGCCTCA 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    126 CCGGCCAATGCCCCAGTGCATACCCCGCCCTTCCTCCCACAAAGAGCACCCCTGCCTCA 185

Qy    181 CAGGTGTATTCCTCAACACCGACTTTGCCTTCCGCCTATACCGCAGGCTGGGTTTTGGAG 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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OM nucleic - nucleic search, using sw model

Run on:　October 9, 2005, 02:01:07 ; Search time 723 Seconds
　　　　　　(without alignments)
　　　　　　10709.574 Million cell updates/sec

Title:　US-09-993-180-1_COPY_68_1375
Perfect score:　1308
Sequence:　1 atgcaaggacaggcaggag.........aaaatcccactaatcctag 1308

Scoring table:　IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched:　4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters:　8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
　　　　　　　　　　Maximum Match 100%
　　　　　　　　　　Listing first 45 summaries

Database :　N Geneseq_16Dec04:*
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　　　　3: geneseqm2000s:*
　　　　4: geneseqm2001as:*
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　　　　6: geneseqm2002as:*
　　　　7: geneseqm2002bs:*
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　　　　9: geneseqm2003bs:*
　　　10: geneseqm2003cs:*
　　　11: geneseqm2003ds:*
　　　12: geneseqm2004as:*
　　　13: geneseqm2004bs:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	ID	Description
1	1308	100.0	1743	3	AAA37089	Aaa37089 Human PRO
2	1308	100.0	1743	4	AAF54367	Aaf54367 Primer #1
3	1308	100.0	1743	4	AAS46150	Aas46150 Human DNA
4	1308	100.0	1743	6	ABL88183	Abl88183 Human PRO
5	1308	100.0	1743	6	ABK11752	Abk11752 cDNA enco
6	1308	100.0	1743	6	ABL95672	Abl95672 Human ang
7	1308	100.0	1743	8	ACA89600	Aca89600 cDNA enco
8	1308	100.0	1743	8	ACA73610	Aca73610 Human sec
9	1308	100.0	1743	8	ACA05925	Aca05925 Human sec
10	1308	100.0	1743	8	ACA66759	Aca66759 cDNA enco
11	1308	100.0	1743	8	ACF20334	Acf20334 Human sec
12	1308	100.0	1743	8	ACF19720	Acf19720 Human sec
13	1308	100.0	1743	8	ACD22008	Acd22008 Human sec
14	1308	100.0	1743	8	ACF13173	Acf13173 Human sec
15	1308	100.0	1743	8	ACD25276	Acd25276 Human sec
16	1308	100.0	1743	8	ACF00325	Acf00325 Human sec
17	1308	100.0	1743	8	ACA72382	Aca72382 Novel hum
18	1308	100.0	1743	8	ACD04906	Acd04906 Novel hum
19	1308	100.0	1743	8	ACD18367	Acd18367 Human sec
20	1308	100.0	1743	8	ACD08374	Acd08374 Human sec
21	1308	100.0	1743	8	ACA88808	Aca88808 Novel hum
22	1308	100.0	1743	8	ACA70250	Aca70250 Human sec
23	1308	100.0	1743	8	ACD12472	Acd12472 Novel hum
24	1308	100.0	1743	8	ACC74387	Acc74387 Human sec
25	1308	100.0	1743	8	ACD16015	Acd16015 Human sec
26	1308	100.0	1743	8	ACD25583	Acd25583 Novel hum
27	1308	100.0	1743	8	ACD18060	Acd18060 Human sec
28	1308	100.0	1743	8	ACC88347	Acc88347 Human sec
29	1308	100.0	1743	8	ACD21701	Acd21701 Human sec
30	1308	100.0	1743	8	ABX98378	Abx98378 Human CDN
31	1308	100.0	1743	8	ACD14129	Acd14129 Human PRO
32	1308	100.0	1743	8	ACD09909	Acd09909 Human sec
33	1308	100.0	1743	8	ACC88654	Acc88654 Human sec
34	1308	100.0	1743	8	ACD21394	Acd21394 Human sec
35	1308	100.0	1743	8	ABX75766	Abx75766 Human CDN
36	1308	100.0	1743	8	ABX97969	Abx97969 Human PRO
37	1308	100.0	1743	8	ACA97445	Aca97445 Novel hum
38	1308	100.0	1743	8	ACA57908	Aca57908 Human PRO
39	1308	100.0	1743	8	ACD14436	Acd14436 Human sec
40	1308	100.0	1743	8	ACC91219	Acc91219 Human sec
41	1308	100.0	1743	8	ACC88961	Acc88961 Human sec
42	1308	100.0	1743	8	ACD07158	Acd07158 Human PRO
43	1308	100.0	1743	8	ACA67609	Aca67609 Human PRO
44	1308	100.0	1743	8	ACC81664	Acc81664 Human sec
45	1308	100.0	1743	8	ACC89268	Acc89268 Human sec

ALIGNMENTS

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ID   AAA37089 standard; cDNA; 1743 BP.
XX
AC   AAA37089;
XX
DT   08-AUG-2000 (first entry)
XX
DE   Human PRO1337 (UNQ692) cDNA sequence SEQ ID NO:235.
XX
KW   Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
KW   transmembrane; secretion; immunoadhesion; pharmaceutical; screening; ss.
XX
OS   Homo sapiens.
XX
PN   WO200012708-A2.
XX
PD   09-MAR-2000.
XX
PF   01-SEP-1999; 99WO-US020111.
XX
PR   01-SEP-1998; 98US-0098716P.
PR   01-SEP-1998; 98US-0098749P.
PR   01-SEP-1998; 98US-0098750P.
PR   01-SEP-1998; 98US-0098803P.
PR   02-SEP-1998; 98US-0098821P.
PR   02-SEP-1998; 98US-0098843P.
PR   09-SEP-1998; 98US-0099536P.
PR   09-SEP-1998; 98US-0099596P.
PR   09-SEP-1998; 98US-0099598P.
PR   09-SEP-1998; 98US-0099602P.
PR   09-SEP-1998; 98US-0099642P.
PR   10-SEP-1998; 98US-0099741P.
PR   10-SEP-1998; 98US-0099754P.
PR   10-SEP-1998; 98US-0099763P.
PR   10-SEP-1998; 98US-0099792P.
PR   10-SEP-1998; 98US-0099808P.
PR   10-SEP-1998; 98US-0099812P.
PR   10-SEP-1998; 98US-0099815P.
PR   10-SEP-1998; 98US-0099816P.
PR   15-SEP-1998; 98US-0100385P.
PR   15-SEP-1998; 98US-0100388P.
PR   15-SEP-1998; 98US-0100390P.

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OM nucleic - nucleic search, using sw model

Run on:       October  9, 2005, 03:00:48 ; Search time 4041 Seconds
                                            (without alignments)
                                            12320.729 Million cell updates/sec

Title:        US-09-993-180-1_COPY_68_1375
Perfect score: 1308
Sequence:     1 atgcaaggacagggcaggag.........aaaatcccactaaatcctag 1308

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched:     3239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters:    68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    EST:*
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              2: gb_est2:*
              3: gb_htc:*
              4: gb_est3:*
              5: gb_est4:*
              6: gb_est5:*
              7: gb_est6:*
              8: gb_gss1:*
              9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1244.4	95.1	1254	9	AY401148	AY401148 Homo sapi
2	1140.6	87.2	1228	9	AY401149	AY401149 Pan trogl
3	742.6	56.8	906	4	BG758811	BG758811 602713172
4	735	56.2	813	4	BG756763	BG756763 602710234
5	730.4	55.8	1073	4	BM455692	BM455692 AGENCOURT
6	725	55.4	1257	9	AY401150	AY401150 Mus muscu
7	725	55.4	1694	3	AK009343	AK009343 Mus muscu
8	708.2	54.1	816	4	BG684028	BG684028 602635635
9	695.6	53.2	946	2	BF794222	BF794222 602255418
10	684	52.3	1097	3	BF975146	BF975146 602244622
11	617.6	47.2	784	4	BG035642	BG035642 602325711
12	612.2	46.8	702	4	BI871087	BI871087 603394260
13	612.2	46.8	771	4	BG398393	BG398393 602439864
14	533.4	40.8	576	2	BF128752	BF128752 601811131
15	440	33.6	447	2	AW408367	AW408367 UI-HF-BK0
16	373.2	28.5	1487	3	CR609815	CR609815 full-leng
17	373.2	28.5	1499	3	CR619614	CR619614 full-leng
18	373.2	28.5	1501	3	CR590750	CR590750 full-leng
19	373.2	28.5	1503	3	CR612671	CR612671 full-leng
20	373.2	28.5	1503	3	CR623490	CR623490 full-leng
21	373.2	28.5	1504	3	CR620654	CR620654 full-leng
22	373.2	28.5	1505	3	CR595639	CR595639 full-leng
23	373.2	28.5	1506	3	CR592388	CR592388 full-leng
24	373.2	28.5	1512	3	CR605766	CR605766 full-leng
25	373.2	28.5	1512	3	CR614066	CR614066 full-leng
26	373.2	28.5	1519	3	CR619948	CR619948 full-leng
27	373.2	28.5	1522	3	CR602814	CR602814 full-leng
28	373.2	28.5	1523	3	CR618899	CR618899 full-leng
29	373.2	28.5	1524	3	CR590774	CR590774 full-leng
30	373.2	28.5	1525	3	CR617878	CR617878 full-leng
31	373.2	28.5	1525	3	CR615154	CR615154 full-leng
32	373.2	28.5	1526	3	CR607384	CR607384 full-leng
33	373.2	28.5	1526	3	CR620688	CR620688 full-leng
34	373.2	28.5	1527	3	CR613551	CR613551 full-leng
35	373.2	28.5	1528	3	CR607976	CR607976 full-leng
36	373.2	28.5	1528	3	CR611190	CR611190 full-leng
37	373.2	28.5	1529	3	CR591314	CR591314 full-leng
38	373.2	28.5	1529	3	CR614583	CR614583 full-leng
39	373.2	28.5	1529	3	CR618039	CR618039 full-leng
40	373.2	28.5	1529	3	CR625124	CR625124 full-leng
41	373.2	28.5	1530	3	CR620316	CR620316 full-leng
42	373.2	28.5	1531	3	CR600352	CR600352 full-leng
43	373.2	28.5	1532	3	CR615849	CR615849 full-leng
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45	373.2	28.5	1534	3	CR620631	CR620631 full-leng

ALIGNMENTS

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RESULT 1
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LOCUS       AY401148        1254 bp    DNA    linear   GSS 12-DEC-2003
DEFINITION  Homo sapiens HCM0794 gene, VIRTUAL TRANSCRIPT, partial sequence,
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ACCESSION   AY401148
VERSION     AY401148.1  GI:39757137
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1254)
AUTHORS     Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
TITLE       Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
JOURNAL     Science 302 (5652), 1960-1963 (2003)
PUBMED      14671302
REFERENCE   2  (bases 1 to 1254)
AUTHORS     Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
TITLE       Direct Submission
JOURNAL     Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
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                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
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     gene            <1..>1254
                     /locus_tag="HCM0794"
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Query Match        95.1%;    Score 1244.4;    DB 9;    Length 1254;
Best Local Similarity   99.5%;   Pred. No. 0;
Matches 1248;   Conservative 0;   Mismatches 6;   Indels 0;   Gaps 0;

Qy     55 ATGGCATCTTACCTTATGGAGTACTCTTTGCTGTTGGCCTCTGCTCCAATCTACTGT 114
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Db      1 ATGGCATCTTACCTTATGGAGTACTCTTTGCTGTTGGCCTCTGCTCCAATCTACTGT 60
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                    GenCore version 5.1.6
          Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:    October  9, 2005, 03:12:08 ; Search time 258 Seconds
                                          (without alignments)
                              8295.542 Million cell updates/sec

Title:          US-09-993-180-1_COPY_68_1375
Perfect score:  1308
Sequence:       1 atgcaaggacaggcaggag........aaaatcccactaaatcctag 1308
Scoring table:  IDENTITY NUC
                Gapop 10.0 , Gapext 1.0
Searched:       1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters:    2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     Issued Patents NA:*
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               2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
               3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
               4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
               5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
               6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                            SUMMARIES
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Result No.	Score	% Query Match	Length	DB	ID	Description
1	1298.4	99.3	1313	4	US-09-774-528-51	Sequence 51, Appl
2	1298.4	99.3	1710	4	US-09-912-628-2	Sequence 2, Appl
3	539.4	41.2	1878	4	US-09-949-016-5670	Sequence 5670, Ap
4	534.6	40.9	1432	4	US-09-919-039-389	Sequence 389, App
5	373.2	28.5	5193	4	US-09-976-594-1126	Sequence 1126, App
6	371.6	28.4	1580	4	US-09-976-594-18	Sequence 18, Appl
7	371.6	28.4	1580	4	US-09-919-039-18	Sequence 18, Appl
8	356.2	27.2	1527	4	US-09-244-111-7	Sequence 7, Appl
9	326.6	25.0	1245	4	US-09-949-016-2272	Sequence 2272, Ap
10	306	23.4	1185	3	US-09-023-339-2	Sequence 2, Appli
11	306	23.4	5932	3	US-09-299-141-4	Sequence 4, Appli
12	306	23.4	6142	3	US-09-299-141-8	Sequence 8, Appli
13	306	23.4	6565	3	US-09-299-141-1	Sequence 1, Appli
14	306	23.4	6714	4	US-09-299-141-6	Sequence 6, Appli
15	306	23.4	6924	3	US-09-299-141-9	Sequence 9, Appli
16	306	23.4	6924	3	US-09-299-141-10	Sequence 10, Appl
17	306	23.4	6924	3	US-09-299-141-11	Sequence 11, Appl
18	306	23.4	6981	4	US-09-299-141-7	Sequence 7, Appli
19	306	23.4	7054	4	US-09-299-141-3	Sequence 3, Appli
20	306	23.4	7405	3	US-09-299-141-2	Sequence 2, Appli
21	304.4	23.3	1417	4	US-10-000-489-91	Sequence 91, Appl
22	289.6	22.1	8190	4	US-09-949-016-17412	Sequence 17412, A
23	288	22.0	1356	1	US-08-002-202-12	Sequence 12, Appl
24	288	22.0	1356	1	US-08-002-202-18	Sequence 18, Appl
25	288	22.0	1356	3	US-08-481-534-12	Sequence 12, Appl
26	288	22.0	1356	1	US-08-481-534-18	Sequence 18, Appl
27	286.4	21.9	1356	1	US-08-002-202-16	Sequence 16, Appl
28	286.4	21.9	1356	3	US-08-481-534-16	Sequence 16, Appl
29	285.8	21.9	1423	1	US-07-829-954-1	Sequence 1, Appl
30	285.8	21.9	1423	1	US-07-994-423-1	Sequence 1, Appli
31	285.8	21.9	1423	1	US-08-421-891-1	Sequence 1, Appli
32	284.2	21.7	1476	4	US-09-949-016-1726	Sequence 1726, Ap
33	271.2	20.7	1266	4	US-09-949-016-2294	Sequence 2294, Ap
34	260	19.9	1194	4	US-10-000-489-49	Sequence 49, Appl
35	254.4	19.4	1263	4	US-09-949-016-834	Sequence 834, App
36	253.8	19.4	1185	3	US-09-023-339-3	Sequence 3, Appli
37	253.8	19.4	1260	3	US-09-023-173-5	Sequence 5, Appli
38	253.8	19.4	1308	3	US-09-023-173-10	Sequence 10, Appl
39	253.8	19.4	1308	3	US-09-023-339-6	Sequence 6, Appli
40	233.4	17.8	1245	4	US-09-755-665-13	Sequence 13, Appl
41	233.4	17.8	1445	4	US-09-461-325-13	Sequence 13, Appl
42	233.4	17.8	1445	4	US-10-012-542-13	Sequence 13, Appl
43	233.4	17.8	1445	4	US-10-115-123-13	Sequence 13, Appl
44	197.6	15.1	1339	1	US-07-859-480-1	Sequence 1, Appli
45	189.2	14.5	8896	4	US-09-949-016-14014	Sequence 14014, A

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ALIGNMENTS

RESULT 1
US-09-774-528-51
; Sequence 51, Application US/09774528
; Patent No. 6743619
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Yang, Yonghong
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wang, Dunrui
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6743619el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 802
; CURRENT APPLICATION NUMBER: US/09/774,528
; CURRENT FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 51
; LENGTH: 1313
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6)...(1313)
US-09-774-528-51

Query Match    99.3%; Score 1298.4; DB 4; Length 1313;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1302; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy     1 ATGCAAGGACAGGGCAGGAGAAGAGGAACCTGCAAAGACATATTTTGTTCCAAAATGGCA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     6 ATGCAAGGACAGGGCAGGAGAAGAGGAACCTGCAAAGACATATTTTGTTCCAAAATGGCA 65

Qy    61 TCTTACCTTTATGGAGTACTCTTGCTTTGGCCTCTGTGTTGCTCCAATCTACTGTGTGTCC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    66 TCTTACCTTTATGGAGTACTCTTGCTTTGGCCTCTGTGTTGCTCCAATCTACTGTGTGTCC 125

Qy   121 CCGGGCCAATGCCCCCAGTGCATACCCCGCCCTTCCTCCACAAAGAGGACACCCCTGCCTCA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   126 CCGGGCCAATGCCCCCAGTGCATACCCCGCCCTTCCTCCACAAAGAGGACACCCCTGCCTCA 185
```

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OM nucleic - nucleic search, using sw model

Run on: October 9, 2005, 04:52:59 ; Search time 912 Seconds
      (without alignments)
      9989.049 Million cell updates/sec

Title: US-09-993-180-1_COPY_68_1375
Perfect score: 1308
Sequence: 1 atgcaaggacaggcaggag........aaatcccactaaatcctag 1308

Scoring table: IDENTITY_NUC
      Gapop 10.0 , Gapext 1.0

Searched: 8443130 seqs, 3482420727 residues

Total number of hits satisfying chosen parameters: 16686260

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
      Maximum Match 100%
      Listing first 45 summaries

Database :   Published Applications NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	DB ID	Description
1	1308	100.0	1743	10	US-09-946-374-235	Sequence 235, App
2	1308	100.0	1743	14	US-10-006-856A-235	Sequence 235, App
3	1308	100.0	1743	14	US-10-184-644-451	Sequence 451, App
4	1308	100.0	1743	14	US-10-006-818A-235	Sequence 235, App
5	1308	100.0	1743	14	US-10-006-485A-235	Sequence 235, App
6	1308	100.0	1743	14	US-10-013-907A-235	Sequence 235, App
7	1308	100.0	1743	14	US-10-015-499A-235	Sequence 235, App
8	1308	100.0	1743	14	US-10-184-634-451	Sequence 451, App
9	1308	100.0	1743	14	US-10-015-393A-235	Sequence 235, App
10	1308	100.0	1743	14	US-10-015-869A-235	Sequence 235, App
11	1308	100.0	1743	14	US-10-012-121A-235	Sequence 235, App
12	1308	100.0	1743	14	US-10-006-116A-235	Sequence 235, App
13	1308	100.0	1743	14	US-10-006-117A-235	Sequence 235, App
14	1308	100.0	1743	14	US-10-017-527A-235	Sequence 235, App
15	1308	100.0	1743	14	US-10-013-913A-235	Sequence 235, App
16	1308	100.0	1743	14	US-10-007-194A-235	Sequence 235, App
17	1308	100.0	1743	14	US-10-013-430A-235	Sequence 235, App
18	1308	100.0	1743	14	US-10-012-671A-235	Sequence 235, App
19	1308	100.0	1743	14	US-10-012-755A-235	Sequence 235, App
20	1308	100.0	1743	14	US-10-015-386A-235	Sequence 235, App
21	1308	100.0	1743	15	US-10-223-085-223	Sequence 223, App
22	1308	100.0	1743	15	US-10-223-084-223	Sequence 223, App
23	1308	100.0	1743	15	US-10-223-088-223	Sequence 223, App
24	1308	100.0	1743	15	US-10-223-090-223	Sequence 223, App
25	1308	100.0	1743	15	US-10-223-087-223	Sequence 223, App
26	1308	100.0	1743	15	US-10-011-692A-235	Sequence 235, App
27	1308	100.0	1743	15	US-10-017-610A-235	Sequence 235, App
28	1308	100.0	1743	15	US-10-006-063A-235	Sequence 235, App
29	1308	100.0	1743	15	US-10-020-063A-235	Sequence 235, App
30	1308	100.0	1743	15	US-10-223-083-223	Sequence 223, App
31	1308	100.0	1743	15	US-10-015-391A-235	Sequence 235, App
32	1308	100.0	1743	15	US-10-223-089-223	Sequence 223, App
33	1308	100.0	1743	15	US-10-015-407A-235	Sequence 235, App
34	1308	100.0	1743	15	US-10-011-833A-235	Sequence 235, App
35	1308	100.0	1743	15	US-10-006-041A-235	Sequence 235, App
36	1308	100.0	1743	15	US-10-015-822A-235	Sequence 235, App
37	1308	100.0	1743	15	US-10-015-387A-235	Sequence 235, App
38	1308	100.0	1743	15	US-10-006-130A-235	Sequence 235, App
39	1308	100.0	1743	15	US-10-006-172A-235	Sequence 235, App
40	1308	100.0	1743	16	US-10-017-253A-235	Sequence 235, App
41	1308	100.0	1743	16	US-10-017-392A-235	Sequence 235, App
42	1308	100.0	1743	16	US-10-017-306A-235	Sequence 235, App
43	1308	100.0	1743	16	US-10-017-867A-235	Sequence 235, App
44	1308	100.0	1743	16	US-10-012-064A-235	Sequence 235, App

ALIGNMENTS

RESULT 1
US-09-946-374-235
; Sequence 235, Application US/09946374
; Publication No.US20030073129A1
GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C1
; CURRENT APPLICATION NUMBER: US/09/946,374

```
                    GenCore version 5.1.6
         Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on:      October  9, 2005, 06:00:34 ; Search time 114.5 Seconds
                                          (without alignments)
                                          8836.377 Million cell updates/sec

Title:         US-09-993-180-1_COPY_68_1375
Perfect score: 2444
Sequence:      1 atgcaaggacagggcaggag.........aaaatcccactaaatcctag 1308

Scoring table: BLOSUM62
               Xgapop 10.0 , Xgapext  0.5
               Ygapop 10.0 , Ygapext  0.5
               Fgapop  6.0 , Fgapext  7.0
               Delop   6.0 , Delext   7.0

Searched:      2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters:      4211384

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/cgm2_1/USPTO_spool_p/US09993180//runat 07102005_180815_18615/app_query.fasta_1.1479
-DB=A_Geneseq_16Dec04 -QFMT=fastan -SUFFIX=n2p.rag -MINMATCH=0.1 -LOOPCU=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09993180 @CGN_1_1.154 @runat 07102005_180815_18615 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A_Geneseq_16Dec04:*
          1: geneseqp1980s:*
          2: geneseqp1990s:*
          3: geneseqp2000s:*
          4: geneseqp2001s:*
          5: geneseqp2002s:*
          6: geneseqp2003as:*
          7: geneseqp2003bs:*
          8: geneseqp2004s:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	2225	91.0	435	5	AAE25298	Human LSI
2	2202	90.1	435	4	AAO14912	Human ser
3	2124	86.9	417	3	AAY99407	Human PRO
4	2124	86.9	417	4	AAB66156	Protein o
5	2124	86.9	417	4	AAU29249	Human PRO
6	2124	86.9	417	5	ABG70636	Human ser
7	2124	86.9	417	5	ABB84928	Human PRO
8	2124	86.9	417	5	AAU77792	Human PRO
9	2124	86.9	417	5	ABB95534	Human ang
10	2124	86.9	417	6	ABU58625	Human PRO
11	2124	86.9	417	6	ABU88173	Abu88173 Novel hum
12	2124	86.9	417	6	ABU84488	Abu84488 Human sec
13	2124	86.9	417	6	ABR66362	Abr66362 Human sec
14	2124	86.9	417	6	ABR65752	Abr65752 Human sec
15	2124	86.9	417	6	ABU99692	Abu99692 Human sec
16	2124	86.9	417	6	ABU82931	Abu82931 Human PRO
17	2124	86.9	417	6	ABU90052	Abu90052 Novel hum
18	2124	86.9	417	6	ABR68301	Abr68301 Human sec
19	2124	86.9	417	6	ABU96354	Abu96354 Novel hum
20	2124	86.9	417	6	ABU92785	Abu92785 Human sec
21	2124	86.9	417	6	ABO08862	Aboo8862 Human sec
22	2124	86.9	417	6	ABO02914	Aboo2914 Human sec
23	2124	86.9	417	6	ABR75068	Abr75068 Human sec
24	2124	86.9	417	6	ABR94830	Abr94830 Human sec
25	2124	86.9	417	6	ABU85803	Abu85803 Human PRO
26	2124	86.9	417	6	ABU98963	Abu98963 Novel hum
27	2124	86.9	417	6	ABU98178	Abu98178 Novel hum
28	2124	86.9	417	6	ABU91884	Abu91884 Novel hum
29	2124	86.9	417	6	ABU89577	Abu89577 Human PRO
30	2124	86.9	417	6	ABU86418	Abu86418 Human sec
31	2124	86.9	417	6	ABU67631	Abu67631 Human sec
32	2124	86.9	417	6	ABU80659	Abu80659 Human PRO
33	2124	86.9	417	6	ABR99577	Abr99577 Human sec
34	2124	86.9	417	6	ABR98967	Abr98967 Human sec
35	2124	86.9	417	6	ABO16490	Abo16490 Human sec
36	2124	86.9	417	6	ABR92390	Abr92390 Human sec
37	2124	86.9	417	6	ABO19031	Abo19031 Human sec
38	2124	86.9	417	6	ABR78452	Abr78452 Human sec
39	2124	86.9	417	6	ABU85188	Abu85188 Novel hum
40	2124	86.9	417	6	ABO00327	Aboo0327 Novel hum
41	2124	86.9	417	6	ABO11659	Abo11659 Human sec
42	2124	86.9	417	6	ABO02304	Aboo2304 Human sec
43	2124	86.9	417	6	ABU88878	Abu88878 Novel hum
44	2124	86.9	417	6	ABU83573	Abu83573 Human sec
45	2124	86.9	417	6	ABO06374	Aboo6374 Novel hum

ALIGNMENTS

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RESULT 1
AAE25298
ID   AAE25298 standard; protein; 435 AA.
XX
AC   AAE25298;
XX
DT   30-OCT-2002 (first entry)
XX
DE   Human LSI-01 protein.
XX
KW   Human; lymphocyte serine protease inhibitor; serpin-01; LSI-01; stroke;
KW   potassium channel beta subunit; cardiovascular; inflammatory disease;
KW   cancer; blood; immune; T-cell malignancy leukaemia; gastrointestinal;
KW   metabolic; proliferative; emphysema; liver cirrhosis; arteriosclerosis;
KW   immunological disorder; rheumatoid arthritis; psoriasis; gene therapy;
KW   autoimmune infertility; vascular disease; microvascular disease; ulcer;
KW   diarrhoea; embolism; thrombosis; neurological; Alzheimer's disease;
KW   epilepsy; cytostatic; hepatotropic; thrombolytic; cerebroprotective;
KW   immunosuppressive; nootropic; neuroprotective; anticonvulsant;
KW   antiinfertility.
XX
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
FT   Peptide        1..38
FT                  /label= Signal-peptide
FT   Protein        39..435
FT                  /note= "Human mature LSI-01 protein"
FT   Binding-site   63..80
FT                  /note= "Heparin binding region; This region is
FT                  specifically referred in claim 34 of the specification"
FT   Binding-site   125..140
FT                  /note= "Heparin binding region; This region is
FT                  specifically referred in claim 34 of the specification"
```

```
                    GenCore version 5.1.6
          Copyright (c) 1993 - 2005 Compugen Ltd.

OM nuclec - protein search, using frame_plus_n2p model

Run on:   October 9, 2005, 14:18:29 ; Search time 34.5 Seconds
                                       (without alignments)
                                       7295.741 Million cell updates/sec

Title:           US-09-993-180-1_COPY_68_1375
Perfect score:   2444
Sequence:        1 atgcaaggacaggcaggag.........aaaatcccccactaaatcctag 1308

Scoring table:   BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop  6.0 , Fgapext 7.0
                 Delop   6.0 , Delext  7.0

Searched:        283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:   566832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US09993180/runat_07102005_180816_18637/app_query.fasta_1.1479
-DB=PIR_79 -QFMT=fastan -SUFFIX=n2p.rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODB=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09993180 @CGN_1_38 @runat_07102005_180816_18637 -NCPU=6 -ICPU=2
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :       PIR_79:*
                 1:  pir1:*
                 2:  pir2:*
                 3:  pir3:*
                 4:  pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	pct	Query Match Length	DB	ID	Description
1	1047		415	2	A47224	thyroxine-binding
2	1044.5		418	2	A39567	thyroxine-binding
3	1029.5		412	2	I46421	thyroxine-binding
4	889.5		427	2	A49518	kallistatin precur
5	852.5		406	2	A39339	protein C inhibito
6	850		433	1	ITHUC	alpha-1-antichymot
7	847		418	2	S23675	contrapsin-related
8	833		418	2	JH0494	alpha-1-antichymot
9	829.5		417	2	S19724	kallikrein-binding
10	829.5		418	1	S31507	serine proteinase
11	821		408	2	S11320	serine proteinase
12	814.5		405	2	A39088	alpha-1-antiprotei
13	806.5		413	2	A54968	alpha-1-antichymot
14	801		413	2	S54981	alpha-1-antiprotei
15	800	32.7	413	2	JX0267	alpha-1-antiprotei
16	799	32.7	403	2	S08102	serine proteinase
17	798	32.7	418	2	JX0129	contrapsin precurs
18	795	32.5	411	1	ITRT	alpha-1-antitrypsi
19	793	32.4	410	2	A45457	alpha 1-proteinase
20	792	32.4	413	2	JX0154	alpha-1-antiprotei
21	790.5	32.3	412	2	S31505	serine proteinase
22	788.5	32.3	406	2	JX0346	alpha-1-antiprotei
23	788	32.2	410	2	C39088	contrapsin precurs
24	787	32.2	416	2	B29131	kallikrein-binding
25	779	31.9	383	2	A36117	corticosteroid-bin
26	779	31.9	416	1	ITSH	alpha-1-antitrypsi
27	778.5	31.8	405	2	A28321	corticosteroid-bin
28	777	31.8	430	2	A49190	corticosteroid-bin
29	774.5	31.7	413	2	I49474	alpha-1 proteinase
30	774.5	31.7	413	1	I56481	alpha 1-proteinase
31	771	31.5	409	1	ITBA	alpha-1-antitrypsi
32	770.5	31.5	413	2	I49470	alpha-1 proteinase
33	769	31.5	416	2	S21097	alpha-1-antitrypsi
34	768.5	31.4	413	2	I49452	alpha-1-antitrypsi
35	768	31.4	418	1	ITHU	alpha-1-antitrypsi
36	767	31.4	413	2	S60036	alpha-1-antitrypsi
37	765.5	31.3	413	2	I49472	alpha-1 proteinase
38	759.5	31.1	413	2	I49473	alpha-1 proteinase
39	757	31.0	406	2	I53281	corticosteroid-bin
40	756.5	31.0	402	2	I49471	alpha-1 proteinase
41	744	30.4	388	2	B39088	alpha-1-antiprotei
42	705.5	28.9	410	2	I50494	serine proteinase
43	697	28.5	412	1	ITMSC	alpha-1-antitrypsi
44	692	28.3	369	2	JH0493	alpha-1-antichymot
45	668	27.3	420	2	A28882	alpha-1-antitrypsi

ALIGNMENTS

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thyroxine-binding globulin precursor - human
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C;Date: 10-May-1996 #sequence_revision 10-May-1996 #text_change 09-Jul-2004
C;Accession: A47224; S39801; A26479; A13535; S22190
R;Hayashi, Y.; Mori, Y.; Janssen, O.E.; Sunthornthepvarakul, T.; Weiss, R.E.; Takeda,
Mol. Endocrinol. 7, 1049-1060, 1993
A;Title: Human thyroxine-binding globulin gene: complete sequence and transcriptional
A;Reference number: A47224; MUID:94049804; PMID:8232304
A;Accession: A47224
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-415 <RES>
A;Cross-references: UNIPROT:P05543; GB:L13470; NID:g405513; PIDN:AAA16067.1; PID:g4055
R;Flink, I.L.; Bailey, T.J.; Gustafson, T.A.; Markham, B.E.; Morkin, E.
Proc. Natl. Acad. Sci. U.S.A. 83, 7708-7712, 1986
A;Title: Complete amino acid sequence of human thyroxine-binding globulin deduced from
A;Reference number: A26479; MUID:87017018; PMID:3094014
A;Accession: A26479
A;Molecule type: mRNA
A;Residues: 1-196, 'T', 198-415 <FLI>
A;Cross-references: GB:M14091; NID:g338696; PIDN:AAA60616.1; PID:g338697
A;Note: the authors translated the codon GAG for residue 94 as Gly
R;Cheng, S.Y.
Biochem. Biophys. Res. Commun. 79, 1212-1218, 1977
A;Reference number: A13535; MUID:78103214; PMID:414747
A;Accession: A13535
A;Molecule type: protein
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                 GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on:   October 9, 2005, 06:04:58 ; Search time 146.5 Seconds
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          Delop   6.0 , Delext   7.0

Searched:      1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters:      3224756

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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                 Listing first 45 summaries

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Database :     UniProt_03:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	2186	89.4	435	2	Q86WD7	Q86wd7 homo sapien
2	2124	86.9	417	2	Q6UWP9	Q6uwp9 homo sapien
3	1867	76.4	370	2	Q86YP7	Q86yp7 homo sapien
4	1690	69.1	337	2	Q86WD5	Q86wd5 homo sapien
5	1640	67.1	335	2	Q86WD6	Q86wd6 homo sapien
6	1473	60.3	334	2	Q86YP6	Q86yp6 homo sapien
7	1429	58.5	286	2	Q86WD4	Q86wd4 homo sapien
8	1347	55.1	418	2	Q9D7D2	Q9d7d2 mus musculu
9	1057.5	43.3	412	1	THBG_PIG	Q9tt35 sus scrofa
10	1047	42.8	415	1	THBG_HUMAN	P05543 homo sapien
11	1044.5	42.7	418	1	THBG_RAT	P35577 rattus norv
12	1042	42.6	415	1	THBG_PANTR	P61640 pan troglod
13	1040.5	42.6	411	1	THBG_BOVIN	Q9tt36 bos taurus
14	1029.5	42.1	412	1	THBG_SHEEP	P50450 ovis aries
15	1021.5	41.8	418	1	THBG_MOUSE	P61939 mus musculu
16	896.5	36.7	440	2	Q86UI7	Q86ui7 homo sapien
17	889.5	36.4	427	1	KAIN_HUMAN	P29622 homo sapien
18	889	36.4	445	1	Q86TR9	Q86tr9 homo sapien
19	872	35.7	423	2	AACT_HUMAN	P01011 homo sapien
20	864.5	35.4	415	2	Q9GMA6	Q9gma6 sus scrofa
21	861.5	35.2	407	1	Q9UNU9	Q9unu9 homo sapien
22	852.5	34.9	406	1	IPSP_HUMAN	P05154 homo sapien
23	847	34.7	418	2	Q03734	Q03734 mus musculu
24	843.5	34.5	405	1	IPSP_MOUSE	P70458 mus musculu
25	842	34.5	424	2	Q8CIE0	Q8cie0 mus musculu
26	841.5	34.4	405	2	Q8BU50	Q8bu50 m mus muscu
27	839	34.3	433	2	Q9YIB8	Q9yib8 xenopus lae
28	838.5	34.3	405	2	Q8BVN1	Q8bvn1 mus musculu
29	837.5	34.3	404	2	Q9N2I2	Q9n2i2 bos taurus
30	837.5	34.3	432	2	Q7SYX0	Q7syx0 xenopus lae
31	834	34.1	418	2	Q91WP6	Q91wp6 mus musculu
32	833	34.1	418	2	Q62258	Q62258 mus musculu
33	831.5	34.0	420	2	Q60552	Q60552 mesocricetu
34	830.5	34.0	413	1	ALMS_TAMSI	Q54758 tamias sibi
35	830.5	34.0	462	2	Q7TPA5	Q7tpa5 rattus norv
36	829.5	33.9	417	2	P29621	P29621 mus musculu
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38	828	33.9	418	1	SI24_APOSY	Q60396 apodemus sy
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43	815.5	33.4	413	1	ALSI_TAMSI	Q76hn9 tamias sibi
44	814.5	33.3	405	1	AIAS_CAVPO	054760 tamias sibi
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ALIGNMENTS

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AC   Q86WD7;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Germinal center B-cell expressed transcript 1 isoform A.
GN   Name=GCET1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22702315; PubMed=12819018;
RA   Pan Z., Shen Y., Du C., Zhou G., Rosenwald A., Staudt L.M.,
RA   Greiner T.C., McKeithan T.W., Chan W.C.;
RT   "Two newly characterized germinal center B-cell-associated genes,
RT   GCET1 and GCET2, have differential expression in normal and neoplastic
RT   B cells.";
RL   Am. J. Pathol. 163:135-144(2003).
CC   -!- SIMILARITY: Belongs to the serpin family.
DR   EMBL; AY220118; AAO65242.1; -.
DR   HSSP; P05154; 1LQ8.
DR   GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR   InterPro; IPR000295; Prot_inh_Lserp2.
DR   InterPro; IPR000215; Prot_inh_serpin.
DR   Pfam; PF00079; Serpin; 1.
DR   PRINTS; PR00780; LEUSERPINII.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; UNKNOWN_1.
KW   Protease inhibitor; Serine protease inhibitor; Serpin.
SQ   SEQUENCE   435 AA;  48569 MW;  21AA8D4B4C4A5983 CRC64;

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Pred. No.:                 6.44e-153        Length:          435
Score:                     2186.00          Matches:         429
Percent Similarity:        98.85%           Conservative:    1
Best Local Similarity:     98.62%           Mismatches:      5
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                          GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on:    October  9, 2005, 14:52:13 ; Search time 34 Seconds
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Title:         US-09-993-180-1_COPY_68_1375
Perfect score: 2444
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Searched:      513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters:    1027090

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1056	43.2	419	4	US-09-949-016-11541	Sequence 11541, A
3	1046	42.8	415	4	US-09-919-039-390	Sequence 390, App
4	889	36.4	422	4	US-09-244-111-8	Sequence 8, Appli
5	872	35.7	423	4	US-09-976-594-19	Sequence 19, Appl
6	872	35.7	423	4	US-09-919-039-19	Sequence 19, Appl
7	847.5	34.7	414	1	US-09-949-016-8143	Sequence 8143, Ap
8	778.5	31.9	405	1	US-07-829-954-2	Sequence 2, Appli
9	778.5	31.9	405	1	US-07-994-423-2	Sequence 2, Appli
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11	778.5	31.9	416	4	US-09-949-016-7597	Sequence 7597, Ap
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13		31.4	768	418	1	US-08-477-108A-3	Sequence 3, Appli
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15		31.4	768	418	4	US-10-030-330-3	Sequence 3, Appli
16		31.4	768	418	5	PCT-US93-08322-3	Sequence 3, Appli
17		31.2	763	418	4	US-10-000-489-92	Sequence 92, Appl
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19		31.0	757	394	2	US-08-553-488A-1	Sequence 1, Appl
20		30.9	756	394	1	US-08-002-202-9	Sequence 9, Appl
21		30.9	756	394	1	US-08-481-534-11	Sequence 11, Appl
22		30.9	755	394	3	US-08-481-534-9	Sequence 9, Appl
23		30.9	755	414	3	US-08-002-202-13	Sequence 13, Appl
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25		30.9	754.5	363	4	US-09-755-665-58	Sequence 58, Appl
26		30.9	754	414	1	US-08-002-202-19	Sequence 19, Appl
27		30.9	754	414	1	US-08-481-534-19	Sequence 19, Appl
28		30.7	751	394	1	US-08-002-202-6	Sequence 6, Appli
29		30.7	751	394	3	US-09-023-339-1	Sequence 1, Appli
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31		30.6	749	414	1	US-08-002-202-17	Sequence 17, Appl
32		30.6	749	414	3	US-08-481-534-17	Sequence 17, Appl
33		28.4	694.5	421	4	US-09-949-016-8165	Sequence 8165, Ap
34		28.3	690.5	414	4	US-09-755-665-14	Sequence 14, Appl
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44		22.6	552	499	4	US-09-054-272-36	Sequence 36, Appl
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ALIGNMENTS

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; Sequence 5, Application US/09912628
; Patent No. 6753164
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Human Serpin Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT001P2
; CURRENT APPLICATION NUMBER: US/09/912,628
; CURRENT FILING DATE:  2001-07-26
; PRIOR APPLICATION NUMBER: PCT/US01/02484
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,769
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: PCT/US00/05082
; PRIOR FILING DATE: 2000-02-29
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; SEQ ID NO 5
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;   ORGANISM: Homo sapiens
US-09-912-628-5

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OM nucleic - protein search, using frame_plus_n2p model

GenCore version 5.1.6
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Run on: October 9, 2005, 15:16:48 ; Search time 121 Seconds
(without alignments)
8994.176 Million cell updates/sec

Title: US-09-993-180-1_COPY_68_1375
Perfect score: 2444
Sequence: 1 atgcaaggacaggcaggag........aaaatcccactaaatcctag 1308

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Delop 6.0 , Delext 7.0

Searched: 1854112 seqs, 416015017 residues

Total number of hits satisfying chosen parameters: 3708224

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2225	91.0	435	10	US-09-993-180-2	Sequence 2, Appl1
2	2202	90.1	435	9	US-09-912-628-5	Sequence 5, Appl1
3	2124	86.9	417	10	US-09-946-374-236	Sequence 236, App
4	2124	86.9	417	13	US-10-052-586-452	Sequence 452, App
5	2124	86.9	417	13	US-10-174-590-452	Sequence 452, App
6	2124	86.9	417	14	US-10-176-758-452	Sequence 452, App
7	2124	86.9	417	14	US-10-175-737-452	Sequence 452, App
8	2124	86.9	417	14	US-10-174-581-452	Sequence 452, App
9	2124	86.9	417	14	US-10-176-483-452	Sequence 452, App
10	2124	86.9	417	14	US-10-176-749-452	Sequence 452, App
11	2124	86.9	417	14	US-10-176-914-452	Sequence 452, App
12	2124	86.9	417	14	US-10-176-915-452	Sequence 452, App
13	2124	86.9	417	14	US-10-173-706-452	Sequence 452, App
14	2124	86.9	417	14	US-10-175-738-452	Sequence 452, App
15	2124	86.9	417	14	US-10-175-752-452	Sequence 452, App
16	2124	86.9	417	14	US-10-176-482-452	Sequence 452, App
17	2124	86.9	417	14	US-10-176-757-452	Sequence 452, App
18	2124	86.9	417	14	US-10-176-913-452	Sequence 452, App
19	2124	86.9	417	14	US-10-180-552-452	Sequence 452, App
20	2124	86.9	417	14	US-10-180-557-452	Sequence 452, App
21	2124	86.9	417	14	US-10-173-700-452	Sequence 452, App
22	2124	86.9	417	14	US-10-174-572-452	Sequence 452, App
23	2124	86.9	417	14	US-10-174-579-452	Sequence 452, App
24	2124	86.9	417	14	US-10-174-582-452	Sequence 452, App
25	2124	86.9	417	14	US-10-174-588-452	Sequence 452, App
26	2124	86.9	417	14	US-10-175-739-452	Sequence 452, App
27	2124	86.9	417	14	US-10-175-740-452	Sequence 452, App
28	2124	86.9	417	14	US-10-175-743-452	Sequence 452, App
29	2124	86.9	417	14	US-10-176-488-452	Sequence 452, App
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31	2124	86.9	417	14	US-10-176-747-452	Sequence 452, App
32	2124	86.9	417	14	US-10-176-750-452	Sequence 452, App
33	2124	86.9	417	14	US-10-176-985-452	Sequence 452, App
34	2124	86.9	417	14	US-10-176-987-452	Sequence 452, App
35	2124	86.9	417	14	US-10-176-992-452	Sequence 452, App
36	2124	86.9	417	14	US-10-176-993-452	Sequence 452, App
37	2124	86.9	417	14	US-10-184-658-452	Sequence 452, App
38	2124	86.9	417	14	US-10-176-991-452	Sequence 452, App
39	2124	86.9	417	14	US-10-173-695-452	Sequence 452, App
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41	2124	86.9	417	14	US-10-173-705-452	Sequence 452, App
42	2124	86.9	417	14	US-10-174-576-452	Sequence 452, App
43	2124	86.9	417	14	US-10-174-585-452	Sequence 452, App
44	2124	86.9	417	14	US-10-174-586-452	Sequence 452, App
45	2124	86.9	417	14	US-10-175-747-452	Sequence 452, App

ALIGNMENTS

RESULT 1
US-09-993-180-2
; Sequence 2, Application US/09993180
; Publication No. US20030054445A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN SERPIN SECRETED FROM LYMPI
; TITLE OF INVENTION: CELLS, LSI-01
; FILE REFERENCE: D0051.NP
; CURRENT APPLICATION NUMBER: US/09/993,180
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 60/248,434
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/257,610
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: US 60/282,745
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2